

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/957557
Source: PCT 09
Date Processed by STIC: 10/29/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be downloaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>09/957557</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO		
1 <input type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>.<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>.<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>.<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>.<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (ii) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID.NO where "X" is shown) This sequence is intentionally skipped	
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If Intentional, please insert the following lines for each skipped sequence: <210> sequence id number <400> sequence id number 000	
9 <input checked="" type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>.<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>.<223> section is required when <213> response is Unknown or Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

PCT09

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/857,557

DATE: 10/29/2001
TIME: 13:15:16

Input Set : A:\BB1297 PCT Seq List.txt
Output Set: N:\CRF3\10292001\I857557.raw

3 <110> APPLICANT: E. I. DU PONT DE NEMOURS AND COMPANY
5 <120> TITLE OF INVENTION: PLANT 1-DEOXY-D-XYLULOSE 5-PHOSPHATE REDUCTOISOMERASE
7 <130> FILE REFERENCE: BB1297
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/857,557
C--> 10 <141> CURRENT FILING DATE: 2001-09-22
12 <150> PRIOR APPLICATION NUMBER: 60/110,865
W--> 13 <151> PRIOR FILING DATE: 1998-DECEMBER-04 *Edt date format*
14 <152> PRIOR FILING DATE: 1998-12-04 *1998-12-04*
15 <160> NUMBER OF SEQ ID NOS: 22
17 <170> SOFTWARE: Microsoft Office 97
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 565
21 <212> TYPE: DNA
22 <213> ORGANISM: Zea mays
24 <220> FEATURE:
25 <221> NAME/KEY: unsure
26 <222> LOCATION: (5)..(9)
28 <220> FEATURE:
29 <221> NAME/KEY: unsure
30 <222> LOCATION: (450)
32 <220> FEATURE:
33 <221> NAME/KEY: unsure
34 <222> LOCATION: (549)
36 <400> SEQUENCE: 1

Field 223 is
required

W--> 37 aatgnnnnnna tcaggctgtt acataggggg gcttcattt tacacacccca acctggccta 60
38 gcttacccta ctacactgt gccgattcg gacggcgcg accaccgctc 120
39 ccctccctct cccccctctc gcccagcggc aattaccaca gcctcccccag caagccggga 180
40 tggctgcact caaggcatcg ttccgggggtg agctcagcgc cgcttccttc ctcgactcca 240
41 gcaggggacc tctcgccag cacaaggatgg attttacgtt tcaaaggaaag ggcaaacgag 300
42 ctatccact gagaaggaca tgctgttcta tgcaacaggc tccaccacca gcatggcctg 360
43 ggcgagctgt tgctgagcct ggcggagtc atggatggc ccaaaggccta tctcgattgt 420
W--> 44 tggttcaact ggtccatag gaacacagan attggacatt gttgcggaga atcctgataa 480
45 gttcagagt/ gttgcttctt ctgctggatc caatgtcact cttctagctg atcaggtcaa 540
W--> 46 aacattcana cctaagggtt ttcgg 565

48 <210> SEQ ID NO: 2
49 <211> LENGTH: 63
50 <212> TYPE: PRT
51 <213> ORGANISM: Zea mays
53 <220> FEATURE:
54 <221> NAME/KEY: UNSURE
55 <222> LOCATION: (25)
57 <220> FEATURE:
58 <221> NAME/KEY: UNSURE
59 <222> LOCATION: (58)

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

Field 223 is required

61 <400> SEQUENCE: 2
62 Ala Trp Pro Glu Ser Trp Asp Gly Pro Lys Pro Ile Ser Ile Val Gly
63 1 5 10 15
W--> 65 Ser Thr Gly Ser Ile Gly Thr Gln Xaa Leu Asp Ile Val Ala Glu Asn

Does Not Comply
Corrected Diskette Needed

② Enumerate unknown
on fileable 221, 222 and 223
for protein and nucleotide
sequences.

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Input Set : A:\BB1297 PCT Seq List.txt
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66 20 25 30
68 Pro Asp Lys Phe Arg Val Val Ala Leu Ala Ala Gly Ser Asn Val Thr
69 35 40 45
W--> 71 Leu Leu Ala Asp Gln Val Lys Thr Phe Xaa Pro Lys Leu Val Arg
72 50 55 60
74 <210> SEQ ID NO: 3
75 <211> LENGTH: 868
76 <212> TYPE: DNA
77 <213> ORGANISM: Zea mays
79 <220> FEATURE:
80 <221> NAME/KEY: unsure
81 <222> LOCATION: (343)
83 <220> FEATURE:
84 <221> NAME/KEY: unsure
85 <222> LOCATION: (356)
87 <220> FEATURE:
88 <221> NAME/KEY: unsure
89 <222> LOCATION: (367)
91 <220> FEATURE:
92 <221> NAME/KEY: unsure
93 <222> LOCATION: (789)
95 <220> FEATURE:
96 <221> NAME/KEY: unsure
97 <222> LOCATION: (862)
99 <400> SEQUENCE: 3
100 gatgaattga aagaagcctt ggctgattgc gaagagaagc cagaaattat tcctggggag 60
101 caaggtgtca tagaagttgc tcgccccatcca gatgcagttc cagttgtcac agggatagta 120
102 ggttgtgcag ggctgaagcc tacagttgtc gcaattgaag ctggtaaaga catagcattg 180
103 gcaaaacaaag agacaacttat tgcaggtgtt cctttgtgc ttccctgtc acacaaacac 240
104 aaagtggaaa ttcttccagc tgattctgag cactctgaa tatttcagtg tatacaaggc 300
W--> 105 ttgtccgaag gtgcacttcg tcgcattatt ctaactgcat cagttgtgc tttca~~and~~gac 360
W--> 106 tggcc~~an~~ttg acaggctgaa agatgtaaaa gttgtgcacg ctttaaagca tccaaactgg 420
107 aatatggaa ggaagatcac agtagattct gctactttat tcaacaaggg tttagaagtt 480
108 attgaagcac attattttt tgggtctgaa tatgtatgaca ttgagatgtt gattcaccca 540
109 cagtctatca tacactctat gttgaaacc caggattcat ctgtccttagc tcagttggga 600
110 tggccagata tgcgttacc aatcttatac accttacat ggccagatag gagtcctgag 660
111 cgctgctaat gagaaggccg tggagtttt cattgacgag aagattagct acctggacat 720
112 attcaaggtg gtggagctt catgtaacgc gcatcggAAC a~~g~~ctggtaac aaccgtca~~t~~ 780
W--> 113 ggaggaat~~ng~~ tcattacatc gtggcaagaa tatgcagcat cacaacatct ctggctgagc 840
W--> 114 tgcctgcat atagtctcac anacttgt *or* 868
116 <210> SEQ ID NO: 4
117 <211> LENGTH: 217
118 <212> TYPE: PRT
119 <213> ORGANISM: Zea mays
121 <220> FEATURE:
122 <221> NAME/KEY: UNSURE
123 <222> LOCATION: (115)
125 <220> FEATURE:
126 <221> NAME/KEY: UNSURE

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Input Set : A:\BB1297 PCT Seq List.txt
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127 <222> LOCATION: (119)
129 <220> FEATURE:
130 <221> NAME/KEY: UNSURE
131 <222> LOCATION: (123)
133 <400> SEQUENCE: 4
134 Asp Glu Leu Lys Glu Ala Leu Ala Asp Cys Glu Glu Lys Pro Glu Ile
135 1 5 10 15
137 Ile Pro Gly Glu Gln Gly Val Ile Glu Val Ala Arg His Pro Asp Ala
138 20 25 30
140 Val Thr Val Val Thr Gly Ile Val Gly Cys Ala Gly Leu Lys Pro Thr
141 35 40 45
143 Val Ala Ala Ile Glu Ala Gly Lys Asp Ile Ala Leu Ala Asn Lys Glu
144 50 55 60
146 Thr Leu Ile Ala Gly Gly Pro Phe Val Leu Pro Leu Ala His Lys His
147 65 70 75 80
149 Lys Val Lys Ile Leu Pro Ala Asp Ser Glu His Ser Ala Ile Phe Gln
150 85 90 95
152 Cys Ile Gln Gly Leu Ser Glu Gly Ala Leu Arg Arg Ile Ile Leu Thr
153 100 105 110
W--> 155 Ala Ser Xaa Gly Ala Phe Xaa Asp Trp Pro Xaa Asp Arg Leu Lys Asp ✓
156 115 120 125
158 Val Lys Val Ala Asp Ala Leu Lys His Pro Asn Trp Asn Met Gly Arg
159 130 135 140
161 Lys Ile Thr Val Asp Ser Ala Thr Leu Phe Asn Lys Gly Leu Glu Val
162 145 150 155 160
164 Ile Glu Ala His Tyr Leu Phe Gly Ala Glu Tyr Asp Asp Ile Glu Ile
165 165 170 175
167 Val Ile His Pro Gln Ser Ile Ile His Ser Met Val Glu Thr Gln Asp
168 180 185 190
170 Ser Ser Val Leu Ala Gln Leu Gly Trp Pro Asp Met Arg Leu Pro Ile
171 195 200 205
173 Leu Tyr Thr Leu Ser Trp Pro Asp Arg
174 210 215
176 <210> SEQ ID NO: 5
177 <211> LENGTH: 1901
178 <212> TYPE: DNA
179 <213> ORGANISM: Oryza sativa
181 <400> SEQUENCE: 5
182 acactatgac catgattacg ccaagcgcgc aattaaccct cactaaaggg aacaaaagct 60
183 ggagctccac cgcggggcg gcccgtctag aactagtgg a tccccgggc tgcaggaatt 120
184 cggcacgagg tttaaaccag acgtcgagtc gagcattaac tcagtcaggg tggccatggc 180
185 gctcaaggtc gtctcttcc cccggggactt ggccgcggc tcattcctcg actccaacag 240
186 aggaggagct ttcaaccagc tcaaagtgg a cctccgttt caaacgaggg acagaagagc 300
187 agtttccctg agaaggactt gctgttcaat gcaacaggct ccaccaccag catggcctgg 360
188 tcgagccgtt gttgaacctg ggaggaggc atgggatggc cccaaagccta tctcaattgt 420
189 tggctcaacc ggttcttattg gcacacagac attggacata gttgcggaga atccagataa 480
190 attccgggtt gttgctcttgc tgcgtggctc caatgtgact cttctagctg atcaggtgaa 540
191 aacattcaaa ccaaagcttg ttgctgttaag aatagtgtca tttagttgatg agctaaagga 600
192 agccttagct gattgtgatt ggaagccaga aattattcct ggtgagcaag gtgtcataga 660

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Input Set : A:\BB1297 PCT Seq List.txt
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255	180	185	190
257	Lys Asp Ile Ala Leu Ala Asn Lys Glu Thr Leu Ile Ala Gly Gly Pro		
258	195	200	205
260	Phe Val Leu Pro Leu Ala Gln Lys His Lys Val Lys Ile Leu Pro Ala		
261	210	215	220
263	Asp Ser Glu His Ser Ala Ile Phe Gln Cys Ile Gln Gly Leu Pro Glu		
264	225	230	235
266	Gly Ala Leu Arg Arg Ile Ile Leu Thr Ala Ser Gly Gly Ala Phe Arg		
267	245	250	255
269	Asp Trp Pro Val Asp Lys Leu Lys Glu Val Lys Val Ala Asp Ala Leu		
270	260	265	270
272	Lys His Pro Asn Trp Asn Met Gly Lys Lys Ile Thr Val Asp Ser Ala		
273	275	280	285
275	Thr Leu Phe Asn Lys Gly Leu Glu Val Ile Glu Ala His Tyr Leu Phe		
276	290	295	300
278	Gly Ala Glu Tyr Asp Asp Ile Glu Ile Val Ile His Pro Gln Ser Ile		
279	305	310	315
281	Ile His Ser Met Ile Glu Thr Gln Asp Ser Ser Val Leu Ala Gln Leu		
282	325	330	335
284	Gly Trp Pro Asp Met Arg Ile Pro Thr Leu Tyr Thr Met Ser Trp Pro		
285	340	345	350
287	Asp Arg Ile Tyr Cys Ser Glu Val Thr Trp Pro Arg Leu Asp Leu Cys		
288	355	360	365
290	Lys Leu Gly Ser Leu Thr Phe Lys Ala Pro Asp Asn Val Lys Tyr Pro		
291	370	375	380
293	Ser Met Asp Leu Ala Tyr Ala Ala Gly Arg Ala Gly Gly Thr Met Thr		
294	385	390	395
296	Gly Val Leu Ser Ala Ala Asn Glu Lys Ala Val Glu Leu Phe Ile Asp		
297	405	410	415
299	Glu Lys Ile Gly Tyr Leu Asp Ile Phe Lys Val Val Glu Leu Thr Cys		
300	420	425	430
302	Asp Ala His Arg Asn Glu Leu Val Thr Arg Pro Ser Leu Glu Glu Ile		
303	435	440	445
305	Ile His Tyr Asp Leu Trp Ala Arg Glu Tyr Ala Ala Ser Leu Gln Pro		
306	450	455	460
308	Ser Thr Gly Leu Ser Pro Val Pro Val		
309	465	470	
311	<210> SEQ ID NO: 7		
312	<211> LENGTH: 1592		
313	<212> TYPE: DNA		
314	<213> ORGANISM: Glycine max		
316	<220> FEATURE:		
317	<221> NAME/KEY: unsure		
318	<222> LOCATION: (993)		
320	<220> FEATURE:		
321	<221> NAME/KEY: unsure		
322	<222> LOCATION: (1402)		
324	<400> SEQUENCE: 7		
325	gctgggtcaa ctgaggtat ggctttaat ttgccttctc ccggccaaat gaagccctta	60	

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L:9 M:270 C: Current Application Number differs, Replaced Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:13 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:37 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:37 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:44 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:44 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:46 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:46 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:65 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:65 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:71 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:71 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:105 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:105 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:106 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:106 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:113 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:113 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:114 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:114 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:155 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4
L:155 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:341 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:341 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:348 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:348 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:427 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:427 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:451 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:451 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:521 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
L:521 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:522 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
L:522 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:531 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
L:531 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:532 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
L:532 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:533 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
L:533 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:553 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:10
L:553 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:583 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:10
L:583 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:650 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11
L:650 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:651 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11

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Input Set : A:\BB1297 PCT Seq List.txt
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L:651 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:652 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11
L:652 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:708 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:13
L:708 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:709 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:13
L:709 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:730 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:14
L:730 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:749 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:749 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15